

ABSTRACT

The present invention relates, *e.g.*, to a method for generating and analyzing multi-factorial biological response profiles, comprising (a) exposing each member of a plurality of expression control sequences, each of which is operatively linked to a heterologous reporter sequence, independently, to at least about three stimuli from a first set of stimuli, wherein at least about two of the stimuli in said first set of stimuli are, optionally, combined in an intra-set combinatorial fashion; (b) detecting a first category of responses of said expression control sequences to said stimuli; and (c) generating a response profile for each of said expression control sequences. The method may further comprise (d) exposing each of said members of the plurality of expression control sequences, independently, to one or more additional sets of stimuli, optionally wherein at least about two of the stimuli in each of said additional sets of stimuli are combined in an intra-set combinatorial fashion, in an inter-set combinatorial fashion with set first set of stimuli; (e) detecting the first category of responses of said expression control sequences to the stimuli in d); and (f) generating a response profile for each of said expression control sequences, which includes the responses detected in b) and in e). Raw response profiles are preferably analyzed by multivariate statistical methods, using a computer.

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